

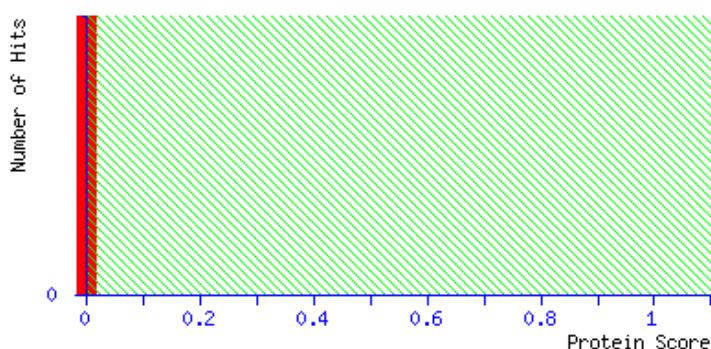


Mascot Search Results

User : Lily-mascot
 Email : l.r.adair@pgr.reading.ac.uk
 Search title : Peptide mix _Ang II_3+ (05072023)
 MS data file : 349.txt
 Database : SwissProt 2021_01 (564277 sequences; 203340877 residues)
 Taxonomy : Eukaryota (eucaryotes) (192754 sequences)
 Timestamp : 5 Jul 2023 at 16:24:53 GMT

Mascot Score Histogram

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
 Individual ions scores > 36 indicate peptides with significant homology.
 Individual ions scores > 50 indicate identity or extensive homology ($p < 0.05$).
 Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As Peptide Summary [Help](#)
 Significance threshold $p < 0.05$ Max. number of hits AUTO
 Standard scoring ☒ MudPIT scoring ☐ Display non-significant matches ☐ Show sub-sets 0
 Show pop-ups ☒ Suppress pop-ups ☐ Sort unassigned Decreasing Score ☐ Require bold red ☐
 Preferred taxonomy All entries
Select All Select None Search Selected ☐ **Error tolerant** Archive Report

No significant hits to report

Peptide matches not assigned to protein hits: (no details means no match)

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> <u>1</u>	1046.5418	1045.5345	1045.5345	0.01	0	33	3.4	1		DRVYIHPF

Search Parameters

Type of search : MS/MS Ion Search
 Enzyme : None
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : ± 10 ppm
 Fragment Mass Tolerance : ± 0.2 Da
 Max Missed Cleavages : 0
 Instrument type : MALDI-QUAD-TOF
 Number of queries : 1

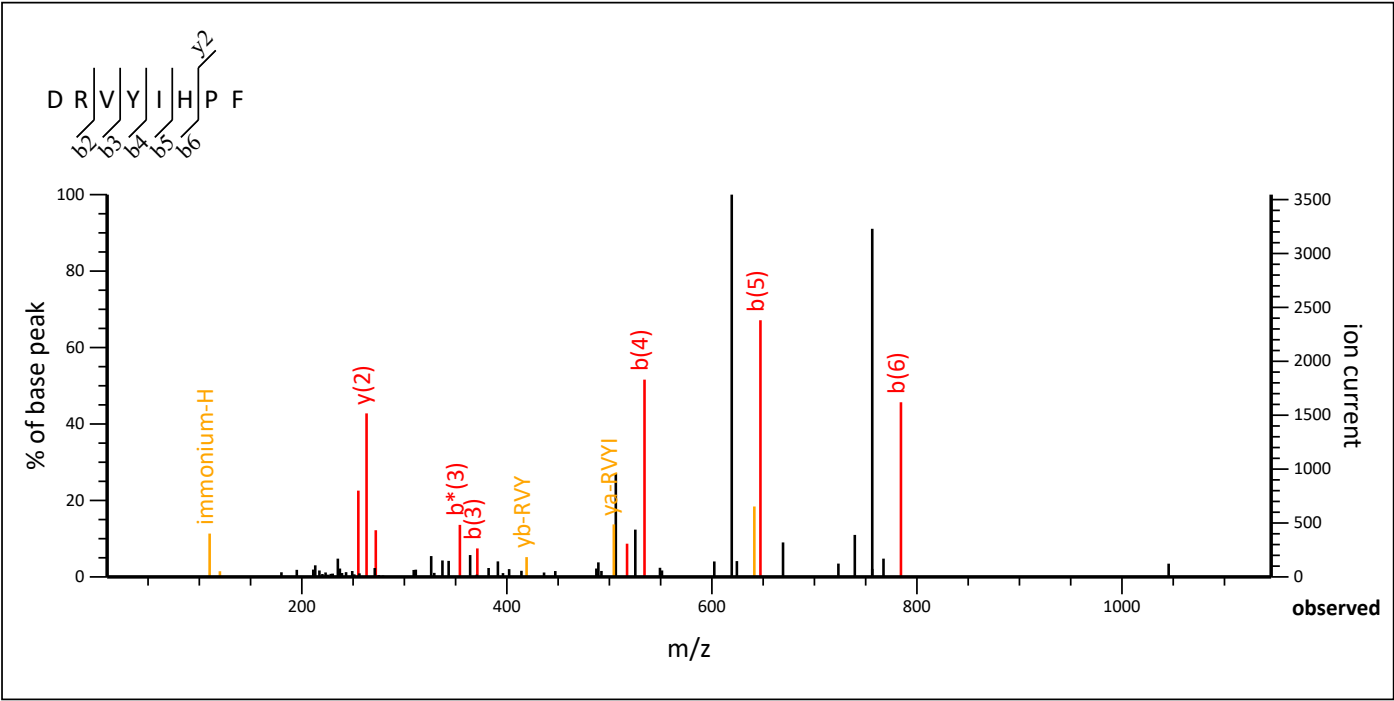
Mascot: <http://www.matrixscience.com/>

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **DRVYIHPF**
Found in **ANGT2_BOTJA** in **SwissProt**, Angiotensin-like peptide 2 (Fragment) OS=Bothrops jararaca OX=8724 PE=1 SV=1

Match to Query 1: 1045.534524 from(1046.541800,1+) intensity(1.0000) index(0)
Title: Reading Top-Down experiment
Data file 349.txt



Navigation icons: ? (help), zoom in, zoom out, reset, and a range selector showing 10.07 to 1145.54.

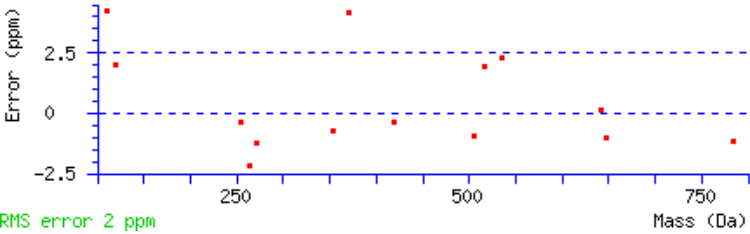
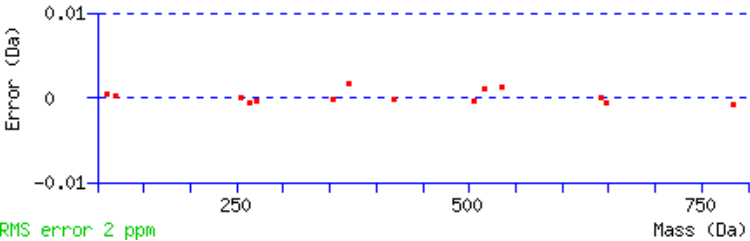
Label all possible matches ☐ Label matches used for scoring ☒

Monoisotopic mass of neutral peptide Mr(calc): 1045.5345
Ions Score: 33 Expect: 3.4
Matches : 15/64 fragment ions using 21 most intense peaks ([help](#))

#	Immon.	b	b*	b ⁰	Seq.	y	y*	#
1	88.0393	116.0342		98.0237	D			8
2	129.1135	272.1353	255.1088	254.1248	R	931.5148	914.4883	7
3	72.0808	371.2037	354.1772	353.1932	V	775.4137		6
4	136.0757	534.2671	517.2405	516.2565	Y	676.3453		5
5	86.0964	647.3511	630.3246	629.3406	I	513.2820		4
6	110.0713	784.4100	767.3835	766.3995	H	400.1979		3
7	70.0651	881.4628	864.4363	863.4522	P	263.1390		2
8	120.0808				F	166.0863		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
RV	228.1819	256.1768	RVY	391.2452	419.2401	RVYI	504.3293	532.3242
RVYIH	641.3882	669.3831	VY	235.1441	263.1390	VYI	348.2282	376.2231
VYIH	485.2871	513.2820	VYIHP	582.3398	610.3348	YI	249.1598	277.1547
YIH	386.2187	414.2136	YIHP	483.2714	511.2663	IHP	223.1553	251.1503

IHP	320.2081	348.2030	HP	207.1240	235.1190			
-----	----------	----------	----	----------	----------	--	--	--



NCBI **BLAST** search of [DRVYIHPF](#)
(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
32.6	1045.5345	0.0000	DRVYIHPF
21.7	1045.5379	-0.0034	YVMKNGVHV
17.2	1045.5267	0.0079	DTFIGLHML
16.6	1045.5444	-0.0099	GIDNLYVGVP
15.8	1045.5379	-0.0033	HLAPDIHMI
14.8	1045.5379	-0.0033	LHDPALHLM
14.4	1045.5305	0.0040	FDSRHLKGS
14.1	1045.5305	0.0041	NERIDRPF
12.6	1045.5404	-0.0058	KNKGDKIDE
12.6	1045.5404	-0.0059	LRTGDKLDE

Mascot: <http://www.matrixscience.com/>